



PCT09

RAW SEQUENCE LISTING

DATE: 02/13/2002

PATENT APPLICATION: US/09/889,926

TIME: 07:25:06

Input Set : A:\2248-115.app

Output Set: N:\CRF3\02132002\I889926.raw

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3 <110> APPLICANT: Xie, Qi
4      Chua, Nam-Hai
5      Institute of Molecular Agrobiolgy, The National U
7 <120> TITLE OF INVENTION: NAC1 - A PLANT GENE ENCODING A TRANSCRIPTION FACTOR
8      INVOLVED IN COTYLEDON AND LATERAL ROOT DEVELOPMENT
10 <130> FILE REFERENCE: 2248-115
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/889,926
C--> 13 <141> CURRENT FILING DATE: 2001-08-18
15 <160> NUMBER OF SEQ ID NOS: 2
17 <170> SOFTWARE: PatentIn Ver. 2.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1287
21 <212> TYPE: DNA
22 <213> ORGANISM: Arabidopsis thaliana
24 <220> FEATURE:
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26 <222> LOCATION: (89)..(1060)
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31 aaaacctaga aaaaaaaagg atcaaatc atg gag acg gaa gaa gag atg aag 112
32                               Met Glu Thr Glu Glu Glu Met Lys
33                               1           5
35 gaa agt agt ata agc atg gtg gag gca aag ttg cct ccg gga ttc aga 160
36 Glu Ser Ser Ile Ser Met Val Glu Ala Lys Leu Pro Pro Gly Phe Arg
37   10           15           20
39 ttt cac ccg aag gac gat gag ctt gtc tgc gat tac ttg atg aga cga 208
40 Phe His Pro Lys Asp Asp Glu Leu Val Cys Asp Tyr Leu Met Arg Arg
41 25           30           35           40
43 tcg ctt cac aat aat cat cga cca cct ctt gtc ctg atc caa gtc gat 256
44 Ser Leu His Asn Asn His Arg Pro Pro Leu Val Leu Ile Gln Val Asp
45           45           50           55
47 ctc aac aag tgt gag cct tgg gac atc cca aaa atg gca tgc gtg gga 304
48 Leu Asn Lys Cys Glu Pro Trp Asp Ile Pro Lys Met Ala Cys Val Gly
49           60           65           70
51 ggg aag gat tgg tat ttc tac agc caa aga gac cga aaa tac gcg acg 352
52 Gly Lys Asp Trp Tyr Phe Tyr Ser Gln Arg Asp Arg Lys Tyr Ala Thr
53           75           80           85
55 ggg ctg aga act aac cga gca acg gcc acc gga tat tgg aaa gcc acc 400
56 Gly Leu Arg Thr Asn Arg Ala Thr Ala Thr Gly Tyr Trp Lys Ala Thr
57           90           95           100
59 ggc aaa gac aga acc att cta aga aag ggt aag cta gtt ggg atg agg 448
60 Gly Lys Asp Arg Thr Ile Leu Arg Lys Gly Lys Leu Val Gly Met Arg
61 105           110           115           120

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63 aag aca ttg gtt ttc tat caa ggt cga gct cct cga ggc cgt aaa acc 496
64 Lys Thr Leu Val Phe Tyr Gln Gly Arg Ala Pro Arg Gly Arg Lys Thr
65 125 130 135
67 gat tgg gtc atg cac gaa ttc cgt ctc caa gga tct cat cat cct ccc 544
68 Asp Trp Val Met His Glu Phe Arg Leu Gln Gly Ser His His Pro Pro
69 140 145 150
71 aat cat tct ctg agc tct cca aag gaa gac tgg gtc ttg tgt agg gta 592
72 Asn His Ser Leu Ser Ser Pro Lys Glu Asp Trp Val Leu Cys Arg Val
73 155 160 165
75 ttc cat aag aat acg gaa gga gtt ata tgt aga gac aac atg gga agc 640
76 Phe His Lys Asn Thr Glu Gly Val Ile Cys Arg Asp Asn Met Gly Ser
77 170 175 180
79 tgt ttt gat gag aca gcc tct gca tcg ctt cct cca ctg atg gat cct 688
80 Cys Phe Asp Glu Thr Ala Ser Ala Ser Leu Pro Pro Leu Met Asp Pro
81 185 190 195 200
83 tac atc aac ttt gac caa gaa ccc tct tct tat ctc agt gat gat cat 736
84 Tyr Ile Asn Phe Asp Gln Glu Pro Ser Ser Tyr Leu Ser Asp Asp His
85 205 210 215
87 cac tac atc atc aat gag cac gta ccc tgc ttc tcc aat ttg tca cag 784
88 His Tyr Ile Ile Asn Glu His Val Pro Cys Phe Ser Asn Leu Ser Gln
89 220 225 230
91 aac caa acc tta aac tcg aac cta acc aac tca gtc tct gaa ctc aag 832
92 Asn Gln Thr Leu Asn Ser Asn Leu Thr Asn Ser Val Ser Glu Leu Lys
93 235 240 245
95 att cca tgc aag aac cct aac ccc ttg ttt act ggt ggt tca gcc tca 880
96 Ile Pro Cys Lys Asn Pro Asn Pro Leu Phe Thr Gly Gly Ser Ala Ser
97 250 255 260
99 gcc acg ctc aca ggc ctc gac tca ttc tgt tct tca gat cag atg gtt 928
100 Ala Thr Leu Thr Gly Leu Asp Ser Phe Cys Ser Ser Asp Gln Met Val
101 265 270 275 280
103 ctc aga gct cta ctc agt cag ctc act aag att gat gga agc ctc ggg 976
104 Leu Arg Ala Leu Leu Ser Gln Leu Thr Lys Ile Asp Gly Ser Leu Gly
105 285 290 295
107 cct aaa gaa tca cag agt tat gga gaa ggt agc tcg gag agc ctc ctg 1024
108 Pro Lys Glu Ser Gln Ser Tyr Gly Glu Gly Ser Ser Glu Ser Leu Leu
109 300 305 310
111 acc gac atc ggt att cca agc act gtt tgg aat tgc tgatgatcga 1070
112 Thr Asp Ile Gly Ile Pro Ser Thr Val Trp Asn Cys
113 315 320
115 gtgtaacgag agttaactatt gctatatcc tatocatgat tggaacaatt cttcgggggg 1130
117 aaataacgtg tgcttgtctg attgtacaaa catttctca ctcttgtacc cacggtagat 1190
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125 <211> LENGTH: 324
126 <212> TYPE: PRT
127 <213> ORGANISM: Arabidopsis thaliana
129 <400> SEQUENCE: 2
130 Met Glu Thr Glu Glu Glu Met Lys Glu Ser Ser Ile Ser Met Val Glu

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136	Val	Cys	Asp	Tyr	Leu	Met	Arg
137		35			40		45
139	Pro	Leu	Val	Leu	Ile	Gln	Val
140		50			55		60
142	Ile	Pro	Lys	Met	Ala	Cys	Val
143	65			70			75
145	Gln	Arg	Asp	Arg	Lys	Tyr	Ala
146			85			90	95
148	Ala	Thr	Gly	Tyr	Trp	Lys	Ala
149		100			105		110
151	Lys	Gly	Lys	Leu	Val	Gly	Met
152		115			120		125
154	Arg	Ala	Pro	Arg	Gly	Arg	Lys
155		130			135		140
157	Leu	Gln	Gly	Ser	His	His	Pro
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160	Glu	Asp	Trp	Val	Leu	Cys	Arg
161			165			170	175
163	Ile	Cys	Arg	Asp	Asn	Met	Gly
164			180			185	190
166	Ser	Leu	Pro	Pro	Leu	Met	Asp
167		195			200		205
169	Ser	Ser	Tyr	Leu	Ser	Asp	Asp
170		210			215		220
172	Pro	Cys	Phe	Ser	Asn	Leu	Ser
173	225			230			235
175	Thr	Asn	Ser	Val	Ser	Glu	Leu
176			245			250	255
178	Leu	Phe	Thr	Gly	Gly	Ser	Ala
179			260			265	270
181	Phe	Cys	Ser	Ser	Asp	Gln	Met
182		275			280		285
184	Thr	Lys	Ile	Asp	Gly	Ser	Leu
185		290			295		300
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VERIFICATION SUMMARY

DATE: 02/13/2002

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TIME: 07:25:07

Input Set : A:\2248-115.app

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L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date